

RAW SEQUENCE LISTING
PATENT APPLICATION US/10/734,126DATE: 08/30/2004
TIME: 14:17:48*pages 1-5 shown.*

INPUT SET: S30662.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

- 1
2
3 (1) General Information:
4 (i) APPLICANT: Plowman, Gregory
5 Mossie, Kevin
6 (ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
7 AND/OR AUR-2 RELATED DISORDERS
8 (iii) NUMBER OF SEQUENCES: 39
9 (iv) CORRESPONDENCE ADDRESS:
10 (A) ADDRESSEE: Lyon & Lyon
11 (B) STREET: 633 West Fifth Street
12 Suite 4700
13 (C) CITY: Los Angeles
14 (D) STATE: California
15 (E) COUNTRY: U.S.A.
16 (F) ZIP: 90071-2066
17 (v) COMPUTER READABLE FORM:
18 (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
19 storage
20 (B) COMPUTER: IBM Compatible
21 (C) OPERATING SYSTEM: IBM P.C. DOS 5.0
22 (D) SOFTWARE: FastSEQ for Windows 2.0
23 (vi) CURRENT APPLICATION DATA:
24 (A) APPLICATION NUMBER: US/10/734,126
25 (B) FILING DATE: 15-Dec-2003
26 (C) CLASSIFICATION: <Unknown>
27 (vii) PRIOR APPLICATION DATA:
28 (A) APPLICATION NUMBER: US/09/784,332
29 (B) FILING DATE: 16-Feb-2001
30
31 (viii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 09/283,011
33 (B) FILING DATE: <Unknown>
34 (A) APPLICATION NUMBER: 09/012,135
35 (B) FILING DATE: January 22, 1998
36 (A) APPLICATION NUMBER: 08/755,728
37 (B) FILING DATE: November 25, 1996
38 (A) APPLICATION NUMBER: 60/023,943
39 (B) FILING DATE: August 14, 1996
40 (A) APPLICATION NUMBER: 60/008,809
41 (B) FILING DATE: December 18, 1995
42 (ix) ATTORNEY/AGENT INFORMATION:
43 (A) NAME: Warburg, Richard J.
44 (B) REGISTRATION NUMBER: 32,327
45 (C) REFERENCE/DOCKET NUMBER: 231/282
46 (x) TELECOMMUNICATION INFORMATION:

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47 (A) TELEPHONE: (213) 489-1600
48 (B) TELEFAX: (213) 955-0440
49 (C) TELEX: 67-3510
50 (2) INFORMATION FOR SEQ ID NO: 1:
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 1244 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: cDNA
57 (iii) HYPOTHETICAL: NO
58 (iv) ANTI-SENSE: NO
59 (vi) ORIGINAL SOURCE:
60 (A) ORGANISM: Homo sapiens
61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
62 CGGGAGAGTA GCAGTGCCTT GGACCCCAGC TCTCCTCCCC CTTTCTCTCT AAGGATGGCC 60
63 CAGAAGGAGA ACTCCTACCC CTGGCCCTAC GGCCGACAGA CGGCTCCATC TGGCCTGAGC 120
64 ACCCTGCCCC AGCGAGTCCT CCGGAAAGAG CCTGTCACCC CATCTGCACT TGTCTCATG 180
65 AGCCGCTCCA ATGTCCAGCC CACAGCTGCC CCTGGCCAGA AGGTGATGGA GAATAGCAGT 240
66 GGGACACCCG ACATCTTAAC GCGGCACCTC ACAATTGATG ACTTTGAGAT TGGGCGTCTT 300
67 CTGGGCAAAG GCAAGTTTGG AAACGTGTAC TTGGCTCGGG AGAAGAAAAG CCATTTCATC 360
68 GTGGCGCTCA AGGTCTCTCT CAAGTCCCAG ATAGAGAAGG AGGGCGTGGA GCATCAGCTG 420
69 CGCAGAGAGA TCGAAATCCA GGCCCACCTG CACCATCCCA ACATCCTGCG TCTCTACAAC 480
70 TATTTTTATG ACCGGAGGAG GATCTACTTG ATTCTAGAGT ATGCCCCCGG CGGGGAGCTC 540
71 TACAAGGAGC TGCAGAAGAG CTGCACATTT GACGAGCAGC GAACAGCCAC GATCATGGAG 600
72 GAGTTGGCAG ATGCTCTAAT GTACTGCCAT GGGAGAAGG TGATTACAG AGACATAAAG 660
73 CCAGAAAATC TGCTCTTAGG GCTCAAGGGA GAGCTGAAGA TTGCTGACTT CGGCTGGTCT 720
74 GTGCATGCGC CCTCCCTGAG GAGGAAGACA ATGTGTGGCA CCCTGGACTA CCTGCCCCCA 780
75 GAGATGATTG AGGGGCGCAT GCACAATGAG AAGGTGGATC TGTGGTGCAT TGGAGTGCTT 840
76 TGCTATGAGC TGCTGGTGGG GAACCCACCC TTCGAGAGTG CATCACACAA CGAGACCTAT 900
77 CGCCGCATCG TCAAGGTGGA CCTAAAGTTC CCCGCTTCTG TGCCACGGG AGCCCAGGAC 960
78 CTCATCTCCA AACTGCTCAG GCATAACCC TCGGAACGGC TGCCCTGGC CCAGGTCTCA 1020
79 GCCCACCTT GGGTCCGGG CAACTCTCGG AGGGTGCTGC CTCCCTCTGC CCTTCAATCT 1080
80 GTCGCTGAT GGTCCCTGTC ATTCACCTCG GTGCGTGTGT TTGTATGTCT GTGTATGTAT 1140
81 AGGGGAAAGA AGGGATCCCT AACTGTTCCC TTATCTGTTT TCTACCTCCT CCTTTGTTTA 1200
82 ATAAAGGCTG AAGCTTTTTG TAAAAAACA AAAAAAAAAA AAAA 1244
83
84 (2) INFORMATION FOR SEQ ID NO: 2:
85 (i) SEQUENCE CHARACTERISTICS:
86 (A) LENGTH: 2198 base pairs
87 (B) TYPE: nucleic acid
88 (C) STRANDEDNESS: single
89 (D) TOPOLOGY: linear
90 (ii) MOLECULE TYPE: cDNA
91 (iii) HYPOTHETICAL: NO
92 (iv) ANTI-SENSE: NO
93 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
94 GGGATATCTC AGTGGCGGAC GAGGACGGCG GGGACAAGGG GCGGCTGGTC GGAGTGGCGG 60
95 ACGTCAAGTC CCCTGTCGGT TCCTCCGTCC CTGAGTGTCC TTGGCGCTGC CTTGTGCCCC 120
96 CCCAGCGCCT TTGCATCCGC TCCTGGGCAC CGAGGCGCCC TGTAGGATAC TGCTTGTATC 180
97 TTATTACAGC TAGAGGCATC ATGGACCGAT CTAAAGAAAA CTGCATTTCA GGACCTGTTA 240
98 AGGCTACAGC TCCAGTTGGA GGTCCAAAAC GTGTTCTCGT GACTCAGCAA TTTCCCTGTG 300
99 AGAATCCATT ACCTGTAAAT AGTGGCCAGG CTCAGCGGGT CTTGTGTCCT TCAAAATCTT 360

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100	CCCAGCGCGT	TCCTTTGCAA	GCACAAAAGC	TTGTCTCCAG	TCACAAGCCG	GTTCAGAATC	420
101	AGAAGCAGAA	GCAATTGCAG	GCAACCAGTG	TACCTCATCC	TGTCTCCAGG	CCACTGAATA	480
102	ACACCCAAAA	GAGCAAGCAG	CCCCTGCCAT	CGGCACCTGA	AAATAATCCT	GAGGAGGAAC	540
103	TGGCATCAAA	ACAGAAAAAT	GAAGAATCAA	AAAAGAGGCA	GTGGGCTTTG	GAAGACTTTG	600
104	AAATTGGTGC	CCCTCTGGGT	AAAGGAAAGT	TTGGTAATGT	TTATTTGGCA	AGAGAAAAGC	660
105	AAAGCAAGTT	TATTCTGGCT	CTTAAAGTGT	TATTTAAAGC	TCAGCTGGAG	AAAGCCGGAG	720
106	TGGAGCATCA	GCTCAGAAGA	GAAGTAGAAA	TACAGTCCCA	CCTTCGGCAT	CCTAATATTC	780
107	TTAGACTGTA	TGGTTATTTT	CATGATGCTA	CCAGAGTCTA	CCTAATTCTG	GAATATGCAC	840
108	CACTTGGAAC	AGTTTATAGA	GAACCTCAGA	AACTTTCAAA	GTTTGATGAG	CAGAGAACTG	900
109	CTACTTATAT	AACAGAATTG	GCAAATGCCC	TGCTTTACTG	TCATTGGAAG	AGAGTTATTC	960
110	ATAGAGACAT	TAAGCCAGAG	AACTTACTTC	TTGGATCAGC	TGGAGAGCTT	AAAATTGCAG	1020
111	ATTTTGGGTG	GTCAGTACAT	GCTCCATCTT	CCAGGAGGAC	CACTCTCTGT	GGCACCCTGG	1080
112	ACTACCTGCC	CCCTGAAATG	ATTGAAGGTC	GGATGCATGA	TGAGAAGGTG	GATCTCTGGA	1140
113	GCCTTGGAGT	TCTTTGCTAT	GAATTTT'AG	TTGGGAAGCC	TCCTTTTGAG	GCAAACACAT	1200
114	ACCAAGAGAC	CTACAAAAGA	ATATCACGGG	TTGAATTCAC	ATTCCCTGAC	TTTGTAAACAG	1260
115	AGGGAGCCAG	GGACCTCATT	TCAAGACTGT	TGAAGCATAA	TCCCAGCCAG	AGGCCAATGC	1320
116	TCAGAGAAGT	ACTTGAACAC	CCCTGGATCA	CAGCAAATTC	ATCAAAACCA	TCAAATTGCC	1380
117	AAAACAAAGA	ATCAGCTAGC	AAACAGTCTT	AGGAATCGTG	CAGGGGGAGA	AATCCTTGAG	1440
118	CCAGGGCTGC	CATATAACCT	GACAGGAACA	TGCTACTGAA	GTTTATTTTA	CCATTGACTG	1500
119	CTGCCCCTCA	TCTAGAACGC	TACACAAGAA	ATATTTGTTT	TACTCAGCAG	GTGTGCCTTA	1560
120	ACCTCCCTAT	TCAGAAAGCT	CCACATCAAT	AAACATGACA	CTCTGAAGTG	AAAGTAGCCA	1620
121	CGAGAATTGT	GCTACTTATA	CTGGTTCATA	ATCTGGAGGC	AAGGTTTCGAC	TGCAGCCGCC	1680
122	CCGTCAGCCT	GTGCTAGGCA	TGGTGTCTTC	ACAGGAGGCA	AATCCAGAGC	CTGGCTGTGG	1740
123	GGAAAGTGAC	CACTCTGCCC	TGACCCCGAT	CAGTTAAGGA	GCTGTGCAAT	AACCTTCCTA	1800
124	GTACCTGAGT	GAGTGTGTAA	CTTATTGGGT	TGGCGAAGCC	TGGTAAAGCT	GT'TGGAATGA	1860
125	GTATGTGATT	CTTTT'AAAGT	ATGAAAATAA	AGATATATGT	ACAGACTTGT	ATTTTTTCTC	1920
126	TGGTGGCATT	CCTTTAGGAA	TGCTGTGTGT	CTGTCCGGCA	CCCCGGTAGG	CCTGATTGGG	1980
127	TTTCTAGTCC	TCCTTAACCA	CTTATCTCCC	ATATGAGAGT	GTGAAAAATA	GGAACACGTG	2040
128	CTCTACTCTC	ATTTAGGGAT	TTGCTTGGGA	TACAGAAGAG	GCCATGTGTC	TCAGAGCTGT	2100
129	TAAGGGCTTA	TTTTTTTAAA	ACATTGGAGT	CATAGCATGT	GTGTAAACTT	TAAATATGCA	2160
130	AATAAATAAG	TATCTATGTC	AAAAAAAAAA	AAAAAAAAA			2198

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

142	Met	Ala	Gln	Lys	Glu	Asn	Ser	Tyr	Pro	Trp	Pro	Tyr	Gly	Arg	Gln	Thr
143	1				5					10					15	
144	Ala	Pro	Ser	Gly	Leu	Ser	Thr	Leu	Pro	Gln	Arg	Val	Leu	Arg	Lys	Glu
145				20					25					30		
146	Pro	Val	Thr	Pro	Ser	Ala	Leu	Val	Leu	Met	Ser	Arg	Ser	Asn	Val	Gln
147			35					40					45			
148	Pro	Thr	Ala	Ala	Pro	Gly	Gln	Lys	Val	Met	Glu	Asn	Ser	Ser	Gly	Thr
149		50					55					60				
150	Pro	Asp	Ile	Leu	Thr	Arg	His	Phe	Thr	Ile	Asp	Asp	Phe	Glu	Ile	Gly
151	65					70					75				80	
152	Arg	Pro	Leu	Gly	Lys	Gly	Lys	Phe	Gly	Asn	Val	Tyr	Leu	Ala	Arg	Glu

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153                                     85                                     90                                     95
154      Lys Lys Ser His Phe Ile Val Ala Leu Lys Val Leu Phe Lys Ser Gln
155                                     100                                     105                                     110
156      Ile Glu Lys Glu Gly Val Glu His Gln Leu Arg Arg Glu Ile Glu Ile
157                                     115                                     120                                     125
158      Gln Ala His Leu His His Pro Asn Ile Leu Arg Leu Tyr Asn Tyr Phe
159                                     130                                     135                                     140
160      Tyr Asp Arg Arg Arg Ile Tyr Leu Ile Leu Glu Tyr Ala Pro Arg Gly
161      145                                     150                                     155                                     160
162      Glu Leu Tyr Lys Glu Leu Gln Lys Ser Cys Thr Phe Asp Glu Gln Arg
163                                     165                                     170                                     175
164      Thr Ala Thr Ile Met Glu Glu Leu Ala Asp Ala Leu Met Tyr Cys His
165                                     180                                     185                                     190
166      Gly Lys Lys Val Ile His Arg Asp Ile Lys Pro Glu Asn Leu Leu Leu
167      195                                     200                                     205
168      Gly Leu Lys Gly Glu Leu Lys Ile Ala Asp Phe Gly Trp Ser Val His
169      210                                     215                                     220
170      Ala Pro Ser Leu Arg Arg Lys Thr Met Cys Gly Thr Leu Asp Tyr Leu
171      225                                     230                                     235                                     240
172      Pro Pro Glu Met Ile Glu Gly Arg Met His Asn Glu Lys Val Asp Leu
173      245                                     250                                     255
174      Trp Cys Ile Gly Val Leu Cys Tyr Glu Leu Leu Val Gly Asn Pro Pro
175      260                                     265                                     270
176      Phe Glu Ser Ala Ser His Asn Glu Thr Tyr Arg Arg Ile Val Lys Val
177      275                                     280                                     285
178      Asp Leu Lys Phe Pro Ala Ser Val Pro Thr Gly Ala Gln Asp Leu Ile
179      290                                     295                                     300
180      Ser Lys Leu Leu Arg His Asn Pro Ser Glu Arg Leu Pro Leu Ala Gln
181      305                                     310                                     315                                     320
182      Val Ser Ala His Pro Trp Val Arg Ala Asn Ser Arg Arg Val Leu Pro
183      325                                     330                                     335
184      Pro Ser Ala Leu Gln Ser Val Ala
185      340
186

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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197      Met Asp Arg Ser Lys Glu Asn Cys Ile Ser Gly Pro Val Lys Ala Thr
198      1                                     5                                     10                                     15
199      Ala Pro Val Gly Gly Pro Lys Arg Val Leu Val Thr Gln Gln Phe Pro
200      20                                     25                                     30
201      Cys Gln Asn Pro Leu Pro Val Asn Ser Gly Gln Ala Gln Arg Val Leu
202      35                                     40                                     45
203      Cys Pro Ser Asn Ser Ser Gln Arg Val Pro Leu Gln Ala Gln Lys Leu
204      50                                     55                                     60
205      Val Ser Ser His Lys Pro Val Gln Asn Gln Lys Gln Lys Gln Leu Gln

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206	65				70				75				80			
207	Ala	Thr	Ser	Val	Pro	His	Pro	Val	Ser	Arg	Pro	Leu	Asn	Asn	Thr	Gln
208					85					90					95	
209	Lys	Ser	Lys	Gln	Pro	Leu	Pro	Ser	Ala	Pro	Glu	Asn	Asn	Pro	Glu	Glu
210				100					105					110		
211	Glu	Leu	Ala	Ser	Lys	Gln	Lys	Asn	Glu	Glu	Ser	Lys	Lys	Arg	Gln	Trp
212				115					120					125		
213	Ala	Leu	Glu	Asp	Phe	Glu	Ile	Gly	Arg	Pro	Leu	Gly	Lys	Gly	Lys	Phe
214				130				135					140			
215	Gly	Asn	Val	Tyr	Leu	Ala	Arg	Glu	Lys	Gln	Ser	Lys	Phe	Ile	Leu	Ala
216						150					155					160
217	Leu	Lys	Val	Leu	Phe	Lys	Ala	Gln	Leu	Glu	Lys	Ala	Gly	Val	Glu	His
218					165					170					175	
219	Gln	Leu	Arg	Arg	Glu	Val	Glu	Ile	Gln	Ser	His	Leu	Arg	His	Pro	Asn
220				180					185					190		
221	Ile	Leu	Arg	Leu	Tyr	Gly	Tyr	Phe	His	Asp	Ala	Thr	Arg	Val	Tyr	Leu
222				195				200						205		
223	Ile	Leu	Glu	Tyr	Ala	Pro	Leu	Gly	Thr	Val	Tyr	Arg	Glu	Leu	Gln	Lys
224			210				215					220				
225	Leu	Ser	Lys	Phe	Asp	Glu	Gln	Arg	Thr	Ala	Thr	Tyr	Ile	Thr	Glu	Leu
226				225			230				235					240
227	Ala	Asn	Ala	Leu	Ser	Tyr	Cys	His	Ser	Lys	Arg	Val	Ile	His	Arg	Asp
228					245					250					255	
229	Ile	Lys	Pro	Glu	Asn	Leu	Leu	Leu	Gly	Ser	Ala	Gly	Glu	Leu	Lys	Ile
230				260					265					270		
231	Ala	Asp	Phe	Gly	Trp	Ser	Val	His	Ala	Pro	Ser	Ser	Arg	Arg	Thr	Thr
232			275					280					285			
233	Leu	Cys	Gly	Thr	Leu	Asp	Tyr	Leu	Pro	Pro	Glu	Met	Ile	Glu	Gly	Arg
234			290				295					300				
235	Met	His	Asp	Glu	Lys	Val	Asp	Leu	Trp	Ser	Leu	Gly	Val	Leu	Cys	Tyr
236			305			310					315					320
237	Glu	Phe	Leu	Val	Gly	Lys	Pro	Pro	Phe	Glu	Ala	Asn	Thr	Tyr	Gln	Glu
238					325					330					335	
239	Thr	Tyr	Lys	Arg	Ile	Ser	Arg	Val	Glu	Phe	Thr	Phe	Pro	Asp	Phe	Val
240				340					345					350		
241	Thr	Glu	Gly	Ala	Arg	Asp	Leu	Ile	Ser	Arg	Leu	Leu	Lys	His	Asn	Pro
242			355				360						365			
243	Ser	Gln	Arg	Pro	Met	Leu	Arg	Glu	Val	Leu	Glu	His	Pro	Trp	Ile	Thr
244			370				375					380				
245	Ala	Asn	Ser	Ser	Lys	Pro	Ser	Asn	Cys	Gln	Asn	Lys	Glu	Ser	Ala	Ser
246			385			390					395					400
247	Lys	Gln	Ser													
248																

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Glu	Asn	Ser	Tyr	Pro	Trp	Pro	Tyr	Gly	Arg	Gln
1				5					10	